

Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 TCGGAGGACAGCAAGCTCCAAAGAGTCACAGAGTCGTGGCCAGTAATGTTAAAGTAGAG 180

QY 181 ACTCAGATGATGAAGAAATGGCGTGCCTGTGAATGAATGGGGAAGAAATGTGCGGAG 240
Db 181 ACTCAGATGATGAAGAAATGGCGTGCCTGTGAATGAATGGGGAAGAAATGTGCGGAG 240

QY 241 GATTTACCAANTGCTGATGCCCTCGGAGAGAAATGAATGGCTCCACAGGGACCAAGGC 300
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QY 361 ATCTGTGGGATCATTGTCATCGGCGCCCAATGTGCTCATGTGTTCAAAAAGAACCCACCT 420
Db 361 ATCTGTGGGATCATTGTCATCGGCGCCCAATGTGCTCATGTGTTCAAAAAGAACCCACCT 420

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QY 1441 CACGGCTTCCGCTGATCTTTGAGTGCACATGTGCGGTACACAGCCAGGACCGGTAC 1500
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QY 1501 GAGTTCCTGCTGCACATACAGCGAGGAGGAGCAGCTTCCACATGAGCTAA 1551
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RESULT 2
S80876
LOCUS
DEFINITION
S80876
ACCESSION
VERSION
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
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source
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/protein_id="AAB50683.1"
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2002, 07:06:00 ; Search time 2044.51 Seconds
(without alignments)
15875.226 Million cell updates/sec

Title: US-08-711-417c-165
Perfect score: 1551
Sequence: 1 ATGATGCTGACGAGGTCA.....ACCGCTTCACATGAGCTAA 1551

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vt.*
- 30: em_hgt_hum.*
- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_hgtgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1551	100.0	1551	6	ARI49755	ARI49755 Sequence
2	1551	100.0	1788	9	S80876	S80876 IKAROS-h1k1
3	1468.8	94.7	3629	9	HSU040462	U040462 Human Ikaro
4	1386	89.4	1386	6	AR049700	AR049700 Sequence
5	1386	89.4	1386	6	ARI25028	ARI25028 Sequence
6	1386	89.4	1386	6	ARI49594	ARI49594 Sequence
7	1210	78.0	3572	9	BC018349	BC018349 Homo sapi
8	1174.8	75.7	2049	6	AR049702	AR049702 Sequence
9	1174.8	75.7	2049	6	ARI25030	ARI25030 Sequence
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13	868	56.0	1004	6	ARI25033	ARI25033 Sequence
14	868	56.0	1004	6	ARI49599	ARI49599 Sequence
15	814.8	52.5	1550	10	MUSIKAROS	L03547 Mouse Ikaro
16	813.2	52.4	1788	6	AR049699	AR049699 Sequence
17	813.2	52.4	1788	6	ARI25027	ARI25027 Sequence
18	813.2	52.4	1788	6	ARI49593	ARI49593 Sequence
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20	689.4	44.4	1296	6	AR049701	AR049701 Sequence
21	689.4	44.4	1296	6	ARI25029	ARI25029 Sequence
22	689.4	44.4	1296	6	ARI49595	ARI49595 Sequence
23	682.6	44.0	2496	5	OMU92201	U92201 Oncorhynch
24	595.6	38.4	684	10	S74708	S74708 Mus musculu
25	577	37.2	1170	6	AR049703	AR049703 Sequence
26	577	37.2	1170	6	ARI25031	ARI25031 Sequence
27	577	37.2	1170	6	ARI49597	ARI49597 Sequence
28	542	34.9	1915	5	AF163770	AF163770 Danio rer
29	520.6	33.6	1287	5	AB060640	AB060640 Seriola q
30	518.2	33.4	2183	5	OMU92200	U92200 Oncorhynch
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32	496.8	32.0	2375	5	AF163848	AF163848 Raja egla
33	479.2	30.9	203352	2	AL596450	AL596450 Mus muscu
34	460.2	29.7	2301	5	OMU92198	U92198 Oncorhynch
35	458.2	29.5	1128	6	AR049704	AR049704 Sequence
36	458.2	29.5	1128	6	ARI25032	ARI25032 Sequence
37	458.2	29.5	1128	6	ARI49598	ARI49598 Sequence
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39	414.6	26.7	2098	5	AF129512	AF129512 Homo sapi
40	412.4	26.6	1672	5	AF163850	AF163850 Raja egla
41	411.8	26.6	1521	10	AF001293	AF001293 Mus muscu
42	409.2	26.4	1876	5	AF163847	AF163847 Raja egla
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44	404.8	26.1	1847	10	AF044257	AF044257 Mus muscu
45	394	25.4	1639	5	AF416371	AF416371 Danio rer

ALIGNMENTS

RESULT 1	ARI49755	ARI49755	Sequence	1551 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	ARI49755	Sequence	165 from patent US 6228611.				
DEFINITION	ARI49755	Sequence	165 from patent US 6228611.				
ACCESSION	ARI49755	Sequence	165 from patent US 6228611.				
VERSION	ARI49755.1	GI:15114346					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 1551)						
AUTHORS	Georgopoulos,K.						
TITLE	Ikaro: A T cell pathway regulatory gene						
JOURNAL	Patent: US 6228611-A 165 08-MAY-2001;						
FEATURES	Location/Qualifiers						
source	1..1551						
BASE COUNT	393 a	450 c	443 g	265 t			
ORIGIN							

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Best Local Similarity 100.0%; Pred. No. 2.5e-250;

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BASE COUNT 450 a 511 c 497 g 330 t
ORIGIN

Query Match 100.0%; Score 1551; DB 9; Length 1788;
Best Local Similarity 100.0%; Pred. No. 2.4e-250;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATGCTGACGAGGGTCAAGACATGCTTTCTCATCAGGGAAGAAAGCCCTCTGTA 60
DB 238 ATGGATGCTGACGAGGGTCAAGACATGCTTTCTCATCAGGGAAGAAAGCCCTCTGTA 297
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DB 298 AGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTCCACACC 357
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QY 241 GATTACGAATGCTGTGATGCTCGGAGAGAAATGAATGGTCCACAGGACCAAGGC 300
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DB 1678 CACGGCTTCGCTGATCCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737
QY 1501 GAGTCTCTGCGACATAACGCGAGGAGGAGCACCCTTCCACATGAGCTAA 1551
DB 1738 GAGTCTCTGCGACATAACGCGAGGAGGAGCACCCTTCCACATGAGCTAA 1788

RESULT 3
HSU40462
LOCUS
DEFINITION Human Ikaros/LyF-1 homolog (hik-1) mRNA, complete cds.
ACCESSION U40462
VERSION U40462.1
KEYWORDS GI:1289370
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3629)
AUTHORS Nietfeld, W. and Meyerhans, A.
TITLE Cloning and sequencing of hik-1, a cDNA encoding a human homologue of mouse Ikaros/LyF-1
JOURNAL Immunol. Lett. 49 (1-2), 139-141 (1996)
MEDLINE 96252222
REFERENCE 2 (bases 1 to 3629)
AUTHORS Nietfeld, W.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1995) Wilfried Nietfeld, Department of Virology, University of Freiburg, Institute for Medical Microbiology and Hygiene, Hermann-Herder-Strasse 11, Freiburg 79104, Germany
FEATURES Location/Qualifiers

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Best Local Similarity 97.7%; Pred. No. 1.3e-236;
Matches 1524; Conservative 0; Mismatches 27; Indels 9; Gaps 3;
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DB 169 ATGGATGCTGATGAGGCTCAAGACATGTCCTCAAGTTTCAGGAAGAAAGCCCCCTGTA 228
QY 61 AGCGATCTCAGATGAGGCGGATGAGCCATGCCGATCCCGAGGAGACTCTCCACCAC 120
DB 229 AGCGATCTCAGATGAGGCGGATGAGCCATGCCGATCCCGAGGAGACTCTCCACCAC 288
QY 121 TCGGAGGACACGACAAAGCTCCAAGATGCAGAGTCTGGCCAGTAATGTTAAAGTAGAG 180
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QY 181 ACTCAGATGATGAAGAAATGGCGTGCCTGTAATGAATGGGGAAGAATGTCGGGAG 240
DB 349 ACTCAGATGATGAAGAAATGGCGTGCCTGTAATGAATGGGGAAGAATGTCGGGAG 408
QY 241 GATTTACGAATGCTTGATGCTCTCGGAGAGAAATGAATGGCTCCACAGGACCAAGGC 300
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DB 529 ATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTATGTTTCACAAAAGAGCCACACT 588
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1386)
AUTHORS Georgopoulos,K.
TITLE Ikaros polypeptides
JOURNAL Patent: US 5824770-A 3 20-Oct-1998;
FEATURES Location/Qualifiers
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source /organism="unknown"
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ORIGIN

Query Match 89.4%; Score 1386; DB 6; Length 1386;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 1386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 226 GAAGAATGTGCGGAGGATTTACGAATGCTTGTGATGCTCGGGAGAGAAAATGAATGCTCC 285
Db 61 GAAGAAATGTGCGGAGGATTTACGAATGCTTGTGATGCTCGGGAGAGAAAATGAATGCTCC 120

QY 286 CACAGGGACCAAGCAGCTCGGCTTTGTCGGGAGTTGGAGGATTCGACTTCTTAACGGA 345
Db 121 CACAGGGACCAAGCAGCTCGGCTTTGTCGGGAGTTGGAGGATTCGACTTCTTAACGGA 180

QY 346 AAACCTAAGTGTGATATCTGTGGGATCAATTCATCGGSCCAATGCTCATGTTTAC 405
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QY 406 AAAAGAAAGCCACTGGAGAACGSCCTTCCAGTGCATGAGTGGGGCCCTCATTCACC 465
Db 241 AAAAGAAAGCCACTGGAGAACGSCCTTCCAGTGCATGAGTGGGGCCCTCATTCACC 300

QY 466 CAGAAAGGCAACCTGTCGGGCACATCAAGCTGCAATTCGGGGAGAGAGCCCTTCAATGC 525
Db 301 CAGAAAGGCAACCTGTCGGGCACATCAAGCTGCAATTCGGGGAGAGAGCCCTTCAATGC 360

QY 526 CACCTCTGCAACTACCGCTGCGCGGAGGAGCGCTCCTACTGGCCCACTGAGGACGCAC 585
Db 361 CACCTCTGCAACTACCGCTGCGCGGAGGAGCGCTCCTACTGGCCCACTGAGGACGCAC 420

QY 586 TCGGTTGGTAAACCTCACAATATGTGATATGTCGCGAAGTATAACAGCGACGCTCT 645
Db 421 TCGGTTGGTAAACCTCACAATATGTGATATGTCGCGAAGTATAACAGCGACGCTCT 480

QY 646 TTAGAGAAACATAAGAGCGCTGCGCACACTACTTGGAAAGCATGGGCTTTCGGGCACA 705
Db 481 TTAGAGAAACATAAGAGCGCTGCGCACACTACTTGGAAAGCATGGGCTTTCGGGCACA 540

QY 706 CTGTACCCAGTCAATTAAGAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAG 765
Db 541 CTGTACCCAGTCAATTAAGAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAG 600

QY 766 ATAGGATCAGAGAGATCTCTGCTGTGACAGACTAGCAAGTAATGTGCGCAACAGTAAG 825
Db 601 ATAGGATCAGAGAGATCTCTGCTGTGACAGACTAGCAAGTAATGTGCGCAACAGTAAG 660

QY 826 AGCTCTATGCTCAGAAATTTCTTGGGACAAAGGCTTGTCCGACAGCGCTTACGACAGT 885
Db 661 AGCTCTATGCTCAGAAATTTCTTGGGACAAAGGCTTGTCCGACAGCGCTTACGACAGT 720

QY 886 GCCAGTACGAGAGGAGAGAAATGATGAAGTCCACCTGATGGACCAAGCCATCAAC 945
Db 721 GCCAGTACGAGAGGAGAGAAATGATGAAGTCCACCTGATGGACCAAGCCATCAAC 780

QY 946 AACGCCATCACTACCTGGGGGCGAGTCCCTGTGCGCCGCTGTGTGAGAGCGCCCGGGC 1005
Db 781 AACGCCATCACTACCTGGGGGCGAGTCCCTGTGCGCCGCTGTGTGAGAGCGCCCGGGC 840

QY 1006 GGTTCGGAGGTGGTCCCGGTATCATCAGCCCGGATGATACAGCGCTCGGAGGC 1065
Db 841 GGTTCGGAGGTGGTCCCGGTATCATCAGCCCGGATGATACAGCGCTCGGAGGC 900

QY 1066 ACCCGCGCTCCAAACCACTCGGCCAGGACAGCGCTGAGTACCTGCTGCTCTCC 1125
Db 901 ACCCGCGCTCCAAACCACTCGGCCAGGACAGCGCTGAGTACCTGCTGCTCTCC 960

QY 1126 AAGCCAAAGTTGGTGGTCCCGGTGAGCGCGGTGCCAGCAACAGCTGCCAAGACTCC 1185
Db 961 AAGCCAAAGTTGGTGGTCCCGGTGAGCGCGGTGCCAGCAACAGCTGCCAAGACTCC 1020

QY 1186 ACGGACACCCGAGAGCAACAAGGAGGACAGCGCGGTCTTATCTACCTGACCAACCAC 1245
Db 1021 ACGGACACCCGAGAGCAACAAGGAGGACAGCGCGGTCTTATCTACCTGACCAACCAC 1080

QY 1246 ATCCGCCGACCGCGCAACCGCTGTGCTCAAGGAGGAGCAGCGCTTACGCTGTG 1305
Db 1081 ATCCGCCGACCGCGCAACCGCTGTGCTCAAGGAGGAGCAGCGCTTACGCTGTG 1140

QY 1306 CGCGCCGCTCCGAGAACTCGCAGGAGCGCTCCGCGTGGTCAGCACACAGCGGGAGCAG 1365
Db 1141 CGCGCCGCTCCGAGAACTCGCAGGAGCGCTCCGCGTGGTCAGCACACAGCGGGAGCAG 1200

QY 1366 ATGAAGGTGTACAAGTCCGAACTACTGCCGGGTGCTCTTCTGGATCAGCTATGTACACC 1425
Db 1201 ATGAAGGTGTACAAGTCCGAACTACTGCCGGGTGCTCTTCTGGATCAGCTATGTACACC 1260

QY 1426 ATCCACATGGCTGCCACGGCTTCCGTGATCCTTTTGTAGTGAACATGTGCGGCTTACCAC 1485
Db 1261 ATCCACATGGCTGCCACGGCTTCCGTGATCCTTTTGTAGTGAACATGTGCGGCTTACCAC 1320

QY 1486 AGCAGGACCGGTACGAGTTCCTGTCGACATTAACGCGGAGGAGCAGCGCTTCCACATG 1545
Db 1321 AGCAGGACCGGTACGAGTTCCTGTCGACATTAACGCGGAGGAGCAGCGCTTCCACATG 1380

QY 1546 AGCTAA 1551
Db 1381 AGCTAA 1386

RESULT 5
LOCUS AR125028 1386 bp DNA Linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6172278.
ACCESSION AR125028
VERSION AR125028.1 GI:14110412
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1386)
AUTHORS Georgopoulos,K.
TITLE Ikaros transgenic cells and mice
JOURNAL Patent: US 6172278-A 2 09-JAN-2001;
FEATURES Location/Qualifiers
1..1386
source /organism="unknown"
BASE COUNT 350 a 403 c 395 g 238 t
ORIGIN

Query Match 89.4%; Score 1386; DB 6; Length 1386;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 1386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AATGTTAAAGTAGAGACTCAGAGTGAAGAGAAATGGCGTGCCTGTGAAATGAATGGG 225
Db 1 AATGTTAAAGTAGAGACTCAGAGTGAAGAGAAATGGCGTGCCTGTGAAATGAATGGG 60

QY 226 GAAGAATGTGCGGAGGATTTACGAATGCTTGTGATGCTCGGGAGAGAAAATGAATGCTCC 285
Db 61 GAAGAATGTGCGGAGGATTTACGAATGCTTGTGATGCTCGGGAGAGAAAATGAATGCTCC 120

QY 1366 ATGAAGTCTACAAGTGCAGACACTGCCGGTGCCTTCTCTGGATCAGCTCATGTACACC 1425
DB 1201 ATGAAGTGTACAAGTGCAGACACTGCCGGTGCCTTCTCTGGATCAGCTCATGTACACC 1260
QY 1426 ATCCACATGGCTGCCACGGCTTCCGTGATCTTTTGTAGTGCACATGTGCGGCTTACCAC 1485
DB 1261 ATCCACATGGCTGCCACGGCTTCCGTGATCTTTTGTAGTGCACATGTGCGGCTTACCAC 1320
QY 1486 AGCCAGGACCGGTACAGTCTCTGTCGCACATAACCGAGGAGGACACCGCTTCCACATG 1545
DB 1321 AGCCAGGACCGGTACAGTCTCTGTCGCACATAACCGAGGAGGACACCGCTTCCACATG 1380
QY 1546 AGCTAA 1551
DB 1381 AGCTAA 1386
RESULT 6
ARL49594 ARL49594 1386 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 3 from patent US 6228611.
DEFINITION ARL49594
ACCESSION ARL49594
VERSION ARL49594.1 GI:15114185
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1386)
AUTHORS Georgopoulos, K.
TITLE Ikaros: A T cell pathway regulatory gene
JOURNAL Patent: US 6228611-A 3 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..1386
BASE COUNT 350 a 403 c 395 g 238 t
ORIGIN

QY 286 CACAGGACCAAGGAGCTCGGCTTGTGGAGTTGGAGGACATTCGACTTCTTAACGGA 345
DB 121 CACAGGACCAAGGAGCTCGGCTTGTGGAGTTGGAGGACATTCGACTTCTTAACGGA 180
QY 346 AAATCTAAAGTGTGATATCTGTGGATCATTTGTCATCGGCGCCCAATGTGCTCATGTTTAC 405
DB 181 AAATCTAAAGTGTGATATCTGTGGATCATTTGTCATCGGCGCCCAATGTGCTCATGTTTAC 240
QY 406 AAAAGAGCCACACTCGGAGACGGCCCTCCAGTGCATATGTCGGGGCCCTCATTCACC 465
DB 241 AAAAGAGCCACACTCGGAGACGGCCCTCCAGTGCATATGTCGGGGCCCTCATTCACC 300
QY 466 CAGAAGGGCAACCTGCTCCGGGCACATCAAGCTGCATTCGGGGAGAACCCCTTCAATGC 525
DB 301 CAGAAGGGCAACCTGCTCCGGGCACATCAAGCTGCATTCGGGGAGAACCCCTTCAATGC 360
QY 526 CACCTCTGCAACTACGCTTCCGGGAGGAGCGCCCTCACTGCGCCACCTGAGGACGAC 585
DB 361 CACCTCTGCAACTACGCTTCCGGGAGGAGCGCCCTCACTGCGCCACCTGAGGACGAC 420
QY 586 TCCGTTGGTAACTCACAATAATGTGGATATTTGGCCGGAAGCTATAAACAGCGAAGCTCT 645
DB 421 TCCGTTGGTAACTCACAATAATGTGGATATTTGGCCGGAAGCTATAAACAGCGAAGCTCT 480
QY 646 TTAGAGGAACATAAAGAGCGCTGCCACACTACTTGGAAAGCATGGCTTCCGGGCACA 705
DB 481 TTAGAGGAACATAAAGAGCGCTGCCACACTACTTGGAAAGCATGGCTTCCGGGCACA 540
QY 706 CTGTACCGATCATTAAGAGAAACTAAAGCAGTGAATGGCAGAGACCTGTGCAAG 765
DB 541 CTGTACCGATCATTAAGAGAAACTAAAGCAGTGAATGGCAGAGACCTGTGCAAG 600
QY 766 ATAGGATCAGAGAGATCTCTGCTGTGGACAGACTAGCAAGTAATGTCGCCAAAGCTAAG 825
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QY 826 AGCTCTATGCTCAGAAATTTCTTGGGCAAGGGGCTGTCCGACACGCGCTTACGACAGT 885
DB 661 AGCTCTATGCTCAGAAATTTCTTGGGCAAGGGGCTGTCCGACACGCGCTTACGACAGT 720
QY 886 GCCACGTACGAGAGAGAGAAATGATGAATGCCACGTGATGACCAAGCCATCAAC 945
DB 721 GCCACGTACGAGAGAGAGAAATGATGAATGCCACGTGATGACCAAGCCATCAAC 780
QY 946 AACGCCATCAACTACCTGGGGGCGAGTCCCTGCGCCGCTGTGTCAGAGCGCCCGGGC 1005
DB 781 AACGCCATCAACTACCTGGGGGCGAGTCCCTGCGCCGCTGTGTCAGAGCGCCCGGGC 840
QY 1006 GGTTCGAGGTGGTCCCGGTCATCAGCCCGATGTACAGCTGCACAGGCGCTCGGAGGGC 1065
DB 841 GGTTCGAGGTGGTCCCGGTCATCAGCCCGATGTACAGCTGCACAGGCGCTCGGAGGGC 900
QY 1066 ACCCGCGCTCCAACTACCTGGGCGGAGGACAGCGCGCTGGAGTACCTGCTGCTCTCC 1125
DB 901 ACCCGCGCTCCAACTACCTGGGCGGAGGACAGCGCGCTGGAGTACCTGCTGCTCTCC 960
QY 1126 AAGGCCAAGTTGGTCCCTTCGAGCGGAGCGGCTCCCGGAGACAGCTGCCAAGACTCC 1185
DB 961 AAGGCCAAGTTGGTCCCTTCGAGCGGAGCGGCTCCCGGAGACAGCTGCCAAGACTCC 1020
QY 1186 ACGGACACCGAGAGAACAAAGAGAGAGCGGAGCGGTCTTACTACCTGACCAACAC 1245
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QY 1246 ATGCGCCGACGCGGCAAGCGGTGCTCAAGGAGGAGACCGCGCTTACGACTGCTG 1305
DB 1081 ATGCGCCGACGCGGCAAGCGGTGCTCAAGGAGGAGACCGCGCTTACGACTGCTG 1140
QY 1306 CCGCGCGCTCCGAGAACTTCGAGGACGCGCTCCGCTGGTTCAGCACAGCGGGGAGCAG 1365
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Query Match 89.4%; Score 1386; DB 6; Length 1386;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 1386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1267 GAGAGCAACAAACGAGGAGCAGCGCTCTATCTACCTGACCAACACCATCGCCCG 1326
 QY 1255 CGCGGC--AACGCGTCTCAAGGAGGAGCAGCGCTCTACCTGCTGCGCGCC 1311
 Db 1327 CACGCGCAACAGGCGTCTCAAGGAGGAGCAGCGCTCTACCTGCTGCGCGCC 1386
 QY 1312 GCCTCCGAGAACTCGCAGGACGCGCTCCCGTGGTCAGCACAGCGGGGAGCAGATGAAG 1371
 Db 1387 GCCTCCGAGAACTCGCAGGACGCGCTCCCGTGGTCAGCACAGCGGGGAGCAGATGAAG 1446
 QY 1372 GTGTACAAAGTCCGAAACACTGCGCGGTCTCTCTGGATCAGTCTATGTACACCATCCAC 1431
 Db 1447 GTGTACAAAGTCCGAAACACTGCGCGGTCTCTCTGGATCAGTCTATGTACACCATCCAC 1506
 QY 1432 ATGGCTGCCACAGGCTTCCCGTGTATCTCTTTAGTCAACATGTGGGCTTACCACAGCCAG 1491
 Db 1507 ATGGCTGCCACAGGCTTCCCGTGTATCTCTTTAGTCAACATGTGGGCTTACCACAGCCAG 1566
 QY 1492 GACCGGTACGAGTCTGTCGACATACGAGGAGGAGCAGCGCTTCCACATGAGCTAA 1551
 Db 1567 GACCGGTACGAGTCTGTCGACATACGAGGAGGAGCAGCGCTTCCACATGAGCTAA 1626

RESULT 8
 AR049702 AR049702 2049 bp DNA linear PAT 29-SEP-1999
 LOCUS Sequence 5 from patent US 5824770.
 DEFINITION AR049702
 ACCESSION AR049702
 VERSION AR049702.1 GI:5971694
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2049)
 AUTHORS Georgopoulos,K.
 TITLE Ikaros polypeptides
 JOURNAL Patent: US 5824770-A 5 20-OCT-1998;
 FEATURES Location/Qualifiers
 source 1..2049
 /organism="unknown"

BASE COUNT 514 a 531 c 574 g 430 t
 ORIGIN

Query Match 75.7%; Score 1174.8; DB 6; Length 2049;
 Best Local Similarity 87.2%; Pred. No. 2.4e-187;
 Matches 1365; Conservative 0; Mismatches 177; Indels 24; Gaps 6;

QY 1 ATGGATGCTGACGAGGCTCAACACATGTCTTCTCATCAGGGAAGAAAGCCCTCTGA 60
 Db 223 ATGGATGCTGATGAGGCTCAAGACATGTCCCAAGTTTCAGGAAAGAGAGCCCTC 282
 QY 61 AGCGATCTCCAGATGAGGCGATGAGCCCATGCCGATCCCGAGGAGCTCTCCACACC 120
 Db 283 AGTGACACTCCAGTGAAGGGATGAGCCCATGCCCTGCTCCCTGAGGAGCTGTCCACTAC 342
 QY 121 TCGGGAGGACAGAAAGCTCCAAAGATGACAGAGTCTGCGCCAGTAATGTTAAAGTAGAG 180
 Db 343 TCTGGAGCACAGCAGAACTCCAAAGATGATGAGGAGTCCCAAGAGTGAATGTTAAAGTAGAG 402
 QY 181 ACTCAGAGTATGAAGAGATGGCGTGTGCTGTGAAATGAATGTTAAAGTAGAGTGTGCGGAG 240
 Db 403 ACTCAGAGTATGAAGAGATGGCGTGTGCTGTGAAATGAATGTTAAAGTAGAGTGTGCGGAG 462
 QY 241 GATTTCAGAAATGCTTGTATGCTCGGAGAGAAATGAATGTTAAAGTAGAGTGTGCGGAG 300
 Db 463 GATTTCAGAAATGCTTGTATGCTCGGAGAGAAATGAATGTTAAAGTAGAGTGTGCGGAG 522
 QY 301 AGCTCGGCTTGTGCGGAGTGTGAGGAGTTCGACTTCCTAACGGAAGAACTAAAGTGTGAT 360
 Db 523 AGCTCGGCTTGTGCGGAGTGTGAGGAGTTCGACTTCCTAACGGAAGAACTAAAGTGTGAT 582
 QY 361 ATCTGTGGGATCAATTTGCATCGGGGCCCAATGTGCTCATGTTTACAAAGAACCCACT 420

Db 313 TCGGAGGACAGCAAGCTCCAGAGTGACAGATCGTGCGCCAGTAATGTTAAAGTAGAG 372
 QY 181 ACTCAGAGTATGAAGAGATGGCGTGTGCTGTGAATGAATGGGAGAAATGTCGGAG 240
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 QY 241 GATTTCAGAAATGCTTGTATGCTCGGAGAGAAATGAATGGCTTCCACAGGAGCAAGGC 300
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 QY 361 ATCTGTGGGATCAATTTGCATCGGGCCCAATGTGCTCATGTTTACAAAGAACCCACT 420
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 Db 613 GGAGAACGGCCCTTCCAGTGAATAGTGGCGGCTCTATTCACCCAGAGGAGCAACCTG 672
 QY 481 CTCGCGCACATCAAGCTCAATTCGGGAGAGGCGCTTCAATGCCACCTCTGCAACTAC 540
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 Db 733 GCCTCGCGCGGAGGAGCGCCCTCACTGCGCACCTGAGGAGGCACTCGTGTGTTAAACCT 780
 QY 601 CACAAATGTGGATATTTGTGGCGAAGCTATTAACAGCAAGCTCTTTAGAGGAACATAA 660
 Db 781 ----- 780
 QY 661 GAGCGTGCCACAACTACTTTGAAAGCATGCGCTTCCGGGACACTGTACCCAGTCAATT 720
 Db 781 -----GTCATT 786
 QY 721 AAAGAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 780
 Db 787 AAAGAGAAACTAATCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 846
 QY 781 TCTCTGCTGCTGACAGACTAGCAAGTAATGTGCGCAACGCTTAAGAGCTCTATGCTCTAG 840
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 Db 907 AAATTTCTTGGGACAAAGGCGCTGTGCGACAGCCCTACGACAGT---GCCAGTACGAG 966
 QY 898 AAGGAGAACGAATGATGAAGTCCAGCTGATGGACCAAGCCATCAACACGCCATCAAC 957
 Db 967 AAGGAGAACGAATGATGAAGTCCAGCTGATGGACCAAGCCATCAACACGCCATCAAC 1026
 QY 958 TACCTGGGGCCGAGTCCCTGCGCGCCGCTGTGCGACAGCCCGCGCGGCTTCCGAGGTG 1017
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 Db 1087 GTCCGGGTATCATGCGCGGATGTACAGCTGCACAAGCCGCTCGCGGAGGCAACCCCGCGC 1146
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 Db 1147 TCCAAACCACTCGGCGCAGGACAGCGCGCTGAGTACCTGTGCTCTTCCAGGCGCAAG 1206
 QY 1135 TTGGTGCCTCGGACGCGGAGCTTCCCGAGCAACAGCTGCCAAGACTCCACGGACACC 1194
 Db 1207 TTGGTGCCTCGGACGCGGAGCTTCCCGAGCAACAGCTGCCAAGACTCCACGGACACC 1266
 QY 1195 GAGAGCAACAGGAGGAGCAGCGAGGCTTATCTACCTGACCAACACACATCGCGCGA 1254

Db	1654	GGTGCCATGGTGCCATGGCTTTCGGGATCCCTTTGAGTGTAAACATGTGTGGTTATCAC	1713
QY	1486	AGCCAGGACCGGTACGAGTCTCTGTGCACATACCGGAGGGGAGCACC	1545
Db	1714	AGCCAGGACAGGTACGAGTCTCATCCATATACGCGGGGGAGCATCGTTACACCTG	1773
QY	1546	AGCTAA	1551
Db	1774	AGCTAA	1779
RESULT	9		
LOCUS	ARI25030		
DEFINITION	Sequence 4 from patent US 6172278.	2049 bp	DNA
ACCESSION	ARI25030		linear
VERSION	ARI25030.1	GI:14110418	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2049)		
AUTHORS	Georgopoulos,K.		
TITLE	Ikaros transgenic cells and mice		
JOURNAL	Patent: US 6172278-A 4 09-JAN-2001;		
FEATURES	Location/Qualifiers		
source	1..2049		
BASE COUNT	514 a 531 c 574 g 430 t		
ORIGIN			
Query Match	75.7%;	Score 1174.8;	DB 6;
Best Local Similarity	87.2%;	Pred. No. 2 4e-187;	Length 2049;
Matches 1365;	Conservative 0;	Mismatches 177;	Indels 24;
Gaps			
QY	1	ATGTCATCTGACGAGGTCACAGACATGTCTTCTCATCAGGGAAGAACCCCTGTGA	60
Db	223	ATGATGTCTGATGAGGGTCAAGACATGTCCCAAGTTTCAGGAAAGAGAGCCCCAGTC	282
QY	61	ATCGATATCTCCAGATGAGGGCGATGAGCCCATGCCATGCCATGCCAGAGACCTCTCCACACACC	120
Db	283	AGTGACATCTCCAGATGAGGGGATGAGCCCATGCCCTGCTCCCTGAGAGACCTGTCCACATACC	342
QY	121	TCGGGAGGACACAAAGCTCCAGAGTGACAGTGCCTGGCCAGTAATGTTAAAGTAGAG	180
Db	343	CTTGAGACACAGAGACTCCAGAGTGTATCGAGGATGCCAGTAATGTTAAAGTAGAG	402
QY	181	ACTCAGATGATGAAGAAATGCGCGTGGCTGTGAAATGAATGGGAGAGATGTGGCGAG	240
Db	403	ACTCAGATGATGAAGAAATGCGCGTGGCTGTGAAATGAATGGGAGAGATGTGGCGAG	462
QY	241	GATTTACCAATGCTTGATGCTCGGAGAGAAATGAATGGCTCCACAGGACCAAGGC	300
Db	463	GATTTACCAATGCTTGATGCTCGGAGAGAAATGAATGGCTCCACAGGACCAAGGC	522
QY	301	AGCTCGGCTTTGTGCGGAGTTGAGGACATTCGACATTCCTTAACGGAACCTAAAGTGTGAT	360
Db	523	AGCTCGGCTTTGTGCGGAGTTGAGGACATTCGACATTCCTTAACGGAACCTAAAGTGTGAT	582
QY	361	ATCTGTGGGATCATTTGCATCGGGGCCCAATGTGCTCATGTTTCAAAAAGAACCACT	420
Db	583	ATCTGTGGGATCATTTGCATCGGGGCCCAATGTGCTCATGTTTCAAAAAGAACCACT	542
QY	421	GGAGAACGGCCCTTCAGATGCAATCAGTCGCGGGCCCTCATTCACCNGAAGGCAACCTG	480
Db	643	GGTGAACGGCTTCAGATGCAATCAGTCGCGGGCCCTCATTCACCNGAAGGCAACCTG	702
QY	481	CTCGGCACATCAAGCTGCATTTCCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTAC	540
Db	703	CTCGGCACATCAAGCTGCATTTCCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTAT	762
QY	541	GCCTGCGCGGAGGACGCCCTCACTGGCCACTGAGGACGACATCCGTTGGTAAACCT	600

AR149596	AR149596	2049 bp	DNA	linear	Pat 08-AUG-2000
LOCUS	Sequence 5 from patent US 6228611.				
DEFINITION	Sequence 5 from patent US 6228611.				
ACCESSION	AR149596				
VERSION	AR149596.1	GI:15114187			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2049)				
AUTHORS	Georgopoulos,K.				
TITLE	Ikaros: A r cell pathway regulatory gene				
JOURNAL	Patent: US 6228611-A 5 08-MAY-2001;				
FEATURES	Location/Qualifiers				
	1..2049				
source	/organism="unknown"				
BASE COUNT	514 a 531 c 574 g 430 t				
ORIGIN					
	Query Match	75.7%;	Score 1174.8;	DB 6;	Length 2049;
	Best Local Similarity	87.2%;	Pred.No. 2.4e-187;		
	Matches 1365;	Conservative	0;	Mismatches 177;	Indels 24;
					Gaps
QY	1	ATGCATCTGTCAGGAGGTCAAGACATGTCTTTCTCATCAGGAGAGAAAGCCCCCTGTA	60		
DB	223	ATGGATGTGCATGAGGTCAGACATGTCCCAAGTTTCAGGAAGGAGAGCCCCCACT	282		
QY	61	AGCGATACTCCAGATGAGCGCATGAGCCATGCGCATCCCGAGGACCTCTCCACCAACC	120		
DB	283	AGTGACATCCAGATGAAGGGAATGAGCCATGCTCTCTCTGAGGACCTGTCCACTACC	342		
QY	121	TCGGAGGACAGCAAACTCCAAAGAGTGACAGAGTGTGGCGCATGTAATGTTAAAGTAGAG	180		
DB	343	TCGGAGGACAGCAAACTCCAAAGAGTGATCGAGGATGCGGAGGATGTTAAAGTAGAG	402		
QY	181	ACTCAGATGATGAAGAGATGGCGTCTGTGAAATGAATGGGGAAGAAATGTGCGGAG	240		
DB	403	ACTCAGATGATGAAGAGATGGCGTCTGTGAAATGAATGGGGAAGAAATGTGCGAG	462		
QY	241	GATTTACGAATGCTTGATGCTCGGAGAGAAATGAATGGTCCACAGGACCAAGGC	300		
DB	463	GATTTACGAATGCTTGATGCTCGGAGAGAAATGAATGGTCCACAGGACCAAGGC	522		
QY	301	AGCTCGGCTTTGTCAGGAGTTGAGGATTCGACTTCCTTAACGGAAACTAAAGTGTGAT	360		
DB	523	AGCTCGGCTTTGTCAGGAGTTGAGGATTCGACTTCCTTAACGGAAACTAAAGTGTGAT	582		
QY	361	ATCTGTGGATCATTTGTCATCGGCGCAATGTGCTCATGCTTTCACAAAGAGGCACACT	420		
DB	583	ATCTGTGGATCATTTGTCATCGGCGCAATGTGCTCATGCTTTCACAAAGAGGCACACT	642		
QY	421	GGAGAACGCCCTTCCAGTGAATCAGTGGCGGCGCTTCATTCACCCAGAGGCAACCTG	480		
DB	643	GGTGAACGCCCTTCCAGTGAATCAGTGGCGGCGCTTCATTCACCCAGAGGCAACCTC	702		
QY	481	CTCGGCACATCAAGTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTCAACTAC	540		
DB	703	CTCGGCACATCAAGTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTCAACTAC	762		
QY	541	GCCTGCCCGGAGGAGCCCTCACTGGCCACCTGAGGAGCCACTCCGTTGGTAAACCT	600		
DB	763	GCCTGCCCGGAGGAGCCCTCACTGGCCACCTGAGGAGCCACTCCGTTGGTAAACCT	822		
QY	601	CACAAATGTGGATATTGTGGCGAGCTATAACAGCGAACCTCTTTAGAGGAACATAA	660		
DB	823	CACAAATGTGGATATTGTGGCGAGCTATAACAGCGAACCTCTTTAGAGGAACATAA	882		
QY	661	GAGCGCTGCCACAACTACTTGGAAAGCATGGGCTTCGGGCGACACTGTACCCAGTCAT	720		
DB	883	GAGCGATGCCCAAACTACTTGGAAAGCATGGGCTTCGGGCG- --GTGTCGCCAGTCAT	939		
QY	721	AAAGAAGAAACTAAGCACAGTGAATGCGAGAGACCTGTGCAAGATAGGATCAGAGAGA	780		

QY 1492 GACCGTACGAGTTCGTGCACATAACCGGAGGAGCACCGCTTCCACATGAGCTAA 1551
DB 1498 GACAGGTATGAATTTCTTCCACATAACTCCGAGGGGACCGCTTCCACATGAGTTAA 1557

RESULT 12
AR049705 AR049705 1004 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 8 from patent US 5824770.
DEFINITION AR049705
ACCESSION AR049705
VERSION AR049705.1 GI:5971697
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1004)
AUTHORS Georgopoulos,K.
TITLE Ikaros polypeptides
JOURNAL Patent: US 5824770-A 8 20-OCT-1998;
FEATURES Location/Qualifiers
source 1..1004
BASE COUNT 235 a 328 c 286 g 155 t
ORIGIN

Query Match 56.0%; Score 868; DB 6; Length 1004;
Best Local Similarity 88.8%; Pred. No. 6.2e-136;
Matches 1004; Conservative 0; Mismatches 0; Indels 126; Gaps 1;

QY 421 GGAGAACGGCCCTCCAGTGCATTCGGGGAGAGGCCCTTCAATGCGACCTCTGCAACTAC 540
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DB 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGGCCCTTCAATGCGACCTCTGCAACTAC 540

QY 541 GCCTGCCCGGAGGAGGAGGCCCTCACTGGCCACCTGAGGAGCGCACTCCGTTGGTAAACCT 600
DB 541 GCCTGCCCGGAGGAGGAGGCCCTCACTGGCCACCTGAGGAGCGCACTCCGTTGGTAAACCT 600

QY 601 CACAAATGTGGATATTGTGGCCGAAGCTATTAACAGCGAAGCTCTTTAGAGAAACATAAA 660
DB 601 CACAAATGTGGATATTGTGGCCGAAGCTATTAACAGCGAAGCTCTTTAGAGAAACATAAA 660

QY 661 GAGCGTGCACAACTACTGTTGAAAGCATGGCCCTTCCGGGACACTCTACCCAGTCAAT 720
DB 661 GAGCGTGCACAACTACTGTTGAAAGCATGGCCCTTCCGGGACACTCTACCCAGTCAAT 720

QY 721 AAAGAAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 780
DB 721 AAAGAAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 780

QY 781 TCTCTCGTGTGACAGACTAGCAAGTATGTGCGCAACGTTAAGAGCTCTATGCTCTCAG 840
DB 781 TCTCTCGTGTGACAGACTAGCAAGTATGTGCGCAACGTTAAGAGCTCTATGCTCTCAG 840

QY 841 AAATTTCTTGGGACAAAGGCGCTTCCGACAGCGCCCTACGA ---CAGTCCACGTCAGAG 897
DB 841 AAATTTCTTGGGACAAAGGCGCTTCCGACAGCGCCCTACGA ---CAGTCCACGTCAGAG 897

QY 898 AAGGAGAACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957
DB 898 AAGGAGAACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957

QY 901 AAGGAGAACGAGATAATGACAGACCAATGATGATGATGATGATGATGATGATGATGATG 960
DB 901 AAGGAGAACGAGATAATGACAGACCAATGATGATGATGATGATGATGATGATGATGATG 960

QY 958 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACAGCGCCCGCGGCGGTTCCGAGGTG 1017
DB 958 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACAGCGCCCGCGGCGGTTCCGAGGTG 1017

QY 1018 GTCCCGGTCTATCAGCCGATGTACAGCTGCACAGCGCGCTCGGAGGGCACCC---CGCGC 1074
DB 1018 GTCCCGGTCTATCAGCCGATGTACAGCTGCACAGCGCGCTCGGAGGGCACCC---CGCGC 1074

QY 1075 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1134
DB 1075 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1134

QY 1081 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1140
DB 1081 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1140

QY 1135 TTGGTGGCCCTCGGAGCGGAGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACC 1194
DB 1135 TTGGTGGCCCTCGGAGCGGAGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACC 1194

QY 1195 GAGAGCAACAGGAGGAGGAGCGCGCTGTTTACTTACCTGACCAACACACATCGCCCGA 1254
DB 1195 GAGAGCAACAGGAGGAGGAGCGCGCTGTTTACTTACCTGACCAACACACATCGCCCGA 1254

QY 1201 GAGAGCAATAATAGGAA---CGGAGTGGTTTAAATTTACTTAAACACACATAGGTCCA 1257
DB 1201 GAGAGCAATAATAGGAA---CGGAGTGGTTTAAATTTACTTAAACACACATAGGTCCA 1257

QY 1255 CGCGC---GCAACGCGTGTCTCTCAAGGAGGAGCAGCCGCGCTACGACCTGTGCGGGCC 1311
DB 1255 CGCGC---GCAACGCGTGTCTCTCAAGGAGGAGCAGCCGCGCTACGACCTGTGCGGGCC 1311

QY 1258 CATGCAAGAAATGGCAATATCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1317
DB 1258 CATGCAAGAAATGGCAATATCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1317

QY 1312 GCCTCCGAGAACTCGCAGGAGCGCGCTCGCGTGTGTCAGCACCAGCGGGAGCAGATGAAG 1371
DB 1312 GCCTCCGAGAACTCGCAGGAGCGCGCTCGCGTGTGTCAGCACCAGCGGGAGCAGATGAAG 1371

QY 1318 GGTACTGCAATATCCAGAGATGCTTTCAAAGTGTATCAGCAGCAATGGGAGCAAGTGAGA 1377
DB 1318 GGTACTGCAATATCCAGAGATGCTTTCAAAGTGTATCAGCAGCAATGGGAGCAAGTGAGA 1377

QY 1372 GTGTACAAGTGGGAACACTCGCGGTGCTCTTCTCTGATCAGCTCATGTATACCAATCCAC 1431
DB 1372 GTGTACAAGTGGGAACACTCGCGGTGCTCTTCTCTGATCAGCTCATGTATACCAATCCAC 1431

QY 1432 ATGGGCTGCCAGGCTTCCGCTGATCCTTTTGTAGTGCAACATGTGCGGCTACCAAGCCAG 1491
DB 1432 ATGGGCTGCCAGGCTTCCGCTGATCCTTTTGTAGTGCAACATGTGCGGCTACCAAGCCAG 1491

QY 1438 ATGGGCTGCCAGGCTTCCGCGACCCCTTTTGAATGCAACATGTGTGGCTACCAAGCCAG 1497
DB 1438 ATGGGCTGCCAGGCTTCCGCGACCCCTTTTGAATGCAACATGTGTGGCTACCAAGCCAG 1497

QY 421 GGAGAACGGCCCTCCAGTGCATTCGGGGAGAGGCCCTTCAATGCGACCTCTGCAACTAC 480
DB 421 GGAGAACGGCCCTCCAGTGCATTCGGGGAGAGGCCCTTCAATGCGACCTCTGCAACTAC 480

QY 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGGCCCTTCAATGCGACCTCTGCAACTAC 540
DB 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGGCCCTTCAATGCGACCTCTGCAACTAC 540

QY 541 GCCTGCCCGGAGGAGGAGGCCCTCACTGGCCACCTGAGGAGCGCACTCCGTTGGTAAACCT 600
DB 541 GCCTGCCCGGAGGAGGAGGCCCTCACTGGCCACCTGAGGAGCGCACTCCGTTGGTAAACCT 600

QY 601 CACAAATGTGGATATTGTGGCCGAAGCTATTAACAGCGAAGCTCTTTAGAGAAACATAAA 660
DB 601 CACAAATGTGGATATTGTGGCCGAAGCTATTAACAGCGAAGCTCTTTAGAGAAACATAAA 660

QY 661 GAGCGTGCACAACTACTGTTGAAAGCATGGCCCTTCCGGGACACTCTACCCAGTCAAT 720
DB 661 GAGCGTGCACAACTACTGTTGAAAGCATGGCCCTTCCGGGACACTCTACCCAGTCAAT 720

QY 721 AAAGAAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 780
DB 721 AAAGAAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 780

QY 781 TCTCTCGTGTGACAGACTAGCAAGTATGTGCGCAACGTTAAGAGCTCTATGCTCTCAG 840
DB 781 TCTCTCGTGTGACAGACTAGCAAGTATGTGCGCAACGTTAAGAGCTCTATGCTCTCAG 840

QY 841 AAATTTCTTGGGACAAAGGCGCTTCCGACAGCGCCCTACGA ---CAGTCCACGTCAGAG 897
DB 841 AAATTTCTTGGGACAAAGGCGCTTCCGACAGCGCCCTACGA ---CAGTCCACGTCAGAG 897

QY 898 AAGGAGAACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957
DB 898 AAGGAGAACGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957

QY 901 AAGGAGAACGAGATAATGACAGACCAATGATGATGATGATGATGATGATGATGATGATG 960
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QY 958 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACAGCGCCCGCGGCGGTTCCGAGGTG 1017
DB 958 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACAGCGCCCGCGGCGGTTCCGAGGTG 1017

QY 961 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACAGCGCGCTCGGAGGGCACCC---CGCGC 1074
DB 961 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACAGCGCGCTCGGAGGGCACCC---CGCGC 1074

QY 1018 GTCCCGGTCTATCAGCCGATGTACAGCTGCACAGCGCGCTCGGAGGGCACCC---CGCGC 1074
DB 1018 GTCCCGGTCTATCAGCCGATGTACAGCTGCACAGCGCGCTCGGAGGGCACCC---CGCGC 1074

QY 1075 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1134
DB 1075 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1134

QY 1081 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1140
DB 1081 TCCAAACACTCGGCCAGGAGCGCGCTGGAGTACCTGCTGCTGCTCTCTCCAAAGGCCAAG 1140

QY 1135 TTGGTGGCCCTCGGAGCGGAGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACC 1194
DB 1135 TTGGTGGCCCTCGGAGCGGAGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACC 1194

QY 1195 GAGAGCAACAGGAGGAGGAGCGCGCTGTTTACTTACCTGACCAACACACATCGCCCGA 1254
DB 1195 GAGAGCAACAGGAGGAGGAGCGCGCTGTTTACTTACCTGACCAACACACATCGCCCGA 1254

QY 1201 GAGAGCAATAATAGGAA---CGGAGTGGTTTAAATTTACTTAAACACACATAGGTCCA 1257
DB 1201 GAGAGCAATAATAGGAA---CGGAGTGGTTTAAATTTACTTAAACACACATAGGTCCA 1257

QY 1255 CGCGC---GCAACGCGTGTCTCTCAAGGAGGAGCAGCCGCGCTACGACCTGTGCGGGCC 1311
DB 1255 CGCGC---GCAACGCGTGTCTCTCAAGGAGGAGCAGCCGCGCTACGACCTGTGCGGGCC 1311

QY 1258 CATGCAAGAAATGGCAATATCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1317
DB 1258 CATGCAAGAAATGGCAATATCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1317

QY 1312 GCCTCCGAGAACTCGCAGGAGCGCGCTCGCGTGTGTCAGCACCAGCGGGAGCAGATGAAG 1371
DB 1312 GCCTCCGAGAACTCGCAGGAGCGCGCTCGCGTGTGTCAGCACCAGCGGGAGCAGATGAAG 1371

QY 1318 GGTACTGCAATATCCAGAGATGCTTTCAAAGTGTATCAGCAGCAATGGGAGCAAGTGAGA 1377
DB 1318 GGTACTGCAATATCCAGAGATGCTTTCAAAGTGTATCAGCAGCAATGGGAGCAAGTGAGA 1377

QY 1372 GTGTACAAGTGGGAACACTCGCGGTGCTCTTCTCTGATCAGCTCATGTATACCAATCCAC 1431
DB 1372 GTGTACAAGTGGGAACACTCGCGGTGCTCTTCTCTGATCAGCTCATGTATACCAATCCAC 1431

QY 1432 ATGGGCTGCCAGGCTTCCGCTGATCCTTTTGTAGTGCAACATGTGCGGCTACCAAGCCAG 1491
DB 1432 ATGGGCTGCCAGGCTTCCGCTGATCCTTTTGTAGTGCAACATGTGCGGCTACCAAGCCAG 1491

QY 1438 ATGGGCTGCCAGGCTTCCGCGACCCCTTTTGAATGCAACATGTGTGGCTACCAAGCCAG 1497
DB 1438 ATGGGCTGCCAGGCTTCCGCGACCCCTTTTGAATGCAACATGTGTGGCTACCAAGCCAG 1497

QY 1081 CACTCGGCCAGGACAGCGCCGCTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTG 1140
 DB 535 CACTCGGCCAGGACAGCGCCGCTGGAGTACCTGCTGCTCTCCAAGGCCAAGTTGGTG 594
 QY 1141 CCCTCGGAGCGGAGCGCTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGC 1200
 DB 595 CCCTCGGAGCGGAGCGCTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGC 654
 QY 1201 AACACGAGGAGCAGCGGAGCGGCTTATCTACCTTGACCAACACCATCGCCCGACGCGG 1260
 DB 655 AACACGAGGAGCAGCGGAGCGGCTTATCTACCTTGACCAACACCATCGCCCGACGCGG 714
 QY 1261 CAACGCTGCTGCTCAAGGAGGAGCAGCGGCTTACGACTGCTGCGGCGCGCTCCGAG 1320
 DB 715 CAACGCTGCTGCTCAAGGAGGAGCAGCGGCTTACGACTGCTGCGGCGCGCTCCGAG 774
 QY 1321 AACTCGCAGGAGCGGCTCCGCGTGTGTCAGCACACGAGCGGAGCAGATGAAGGTGTACAAG 1380
 DB 775 AACTCGCAGGAGCGGCTCCGCGTGTGTCAGCACACGAGCGGAGCAGATGAAGGTGTACAAG 834
 QY 1381 TCGCAACTGCTCGGCTGCTCTTCTGATCAGCTCATGTACACCATCCACATGGGCTGC 1440
 DB 835 TCGCAACTGCTCGGCTGCTCTTCTGATCAGCTCATGTACACCATCCACATGGGCTGC 894
 QY 1441 CAGGCTTCCGCTGATCCCTTTTGGTGTGCAACATGTGCGGCTTACACAGCCAGGACCGGTAC 1500
 DB 895 CAGGCTTCCGCTGATCCCTTTTGGTGTGCAACATGTGCGGCTTACACAGCCAGGACCGGTAC 954
 QY 1501 GAGTTCTCGTCCACATATACCGGAGGAGCAGCGCTTCCACATGAGCTA 1550
 DB 955 GAGTTCTCGTCCACATATACCGGAGGAGCAGCGCTTCCACATGAGCTA 1004

RESULT 13
 ARL125033
 LOCUS ARL125033 1004 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 7 from patent US 6172278.
 ACCESSION ARL125033
 VERSION ARL125033.1 GI:14110423
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1004)
 AUTHORS Georgopoulos,K.
 TITLE Ikaros transgenic cells and mice
 JOURNAL Patent: US 6172278-A 7 09-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..1004
 BASE COUNT 235 a 328 c 286 g 155 t
 ORIGIN

Query Match 56.0%; - Score 868; DB 6; Length 1004;
 Best Local Similarity 88.8%; Pred. No. 6.2e-136;
 Matches 1004; Conservative 0; Mismatches 0; Indels 126; Gaps 1;

QY 421 GGAGAACGCCCTTCCAGTGCATATCAGTGGGGGCTCATTTACCCAGAGGGCAACCTG 480
 DB 1 GGAGAACGCCCTTCCAGTGCATATCAGTGGGGGCTCATTTACCCAGAGGGCAACCTG 60
 QY 481 CTCGGCACATCAAGTGCATTCGGGGGAGAACCCCTTCAATGCGACCTCTGCAACTAC 540
 DB 61 CTCGGCACATCAAGTGCATTCGGGGGAGAACCCCTTCAATGCGACCTCTGCAACTAC 120
 QY 541 GCCTGCCCGGAGGAGCGCCCTCACTGGCCACCTCAGGACGACCTCCGTTGGTAACT 600
 DB 121 GCCTGCCCGGAGGAGCGCCCTCACTGGCCACCTCAGGACGACCTCCGTTGGTAACT 168
 QY 601 CACAAATGTGGATATTGTGGCCGAGCTATAAACAGCGAACGCTCTTTAGAGGAACATAAA 660

DB 169 ----- 168
 QY 661 GAGCGCTGCCACAACTACTTGGAAAGCATGGGCTTCCGGGCACACTGTACCCAGTCATT 720
 DB 169 -----GTCAAT 174
 QY 721 AAAGAAGAAACTAAGCACAGTGAATGGCAGAAAGCTGTGCAAGATAGGATCAGAGAGA 780
 DB 175 AAAGAAGAAACTAAGCACAGTGAATGGCAGAAAGCTGTGCAAGATAGGATCAGAGAGA 234
 QY 781 TCTCTGCTGTGACAGACTAGCAAGTAATGTGCCAAAGCTAAGAGCTCTATGCCTCAG 840
 DB 235 TCTCTGCTGTGACAGACTAGCAAGTAATGTGCCAAAGCTAAGAGCTCTATGCCTCAG 294
 QY 841 AAATTTCTTGGGACAAAGGCGCTTCCGACACGCGCTAGCAGAGTCCAGGTACAGAGAAG 900
 DB 295 AAATTTCTTGGGACAAAGGCGCTTCCGACACGCGCTAGCAGAGTCCAGGTACAGAGAAG 354
 QY 901 GAGAAGAAATGATGAAGTCCACAGTGTGACCAAGCCATCAACAAACGCCATCAACTAC 960
 DB 355 GAGAAGAAATGATGAAGTCCACAGTGTGACCAAGCCATCAACAAACGCCATCAACTAC 414
 QY 961 CTGGGGCGGAGTCCCTTGGCGCGCTGTGACAGACGCGCGCGGTTCGAGGTGGTC 1020
 DB 415 CTGGGGCGGAGTCCCTTGGCGCGCTGTGACAGACGCGCGCGGTTCGAGGTGGTC 474
 QY 1021 CCGGTCTCAGCCCGGATGTACAGCTGTGACAGCGCTGCGAGGGGACCCCGCGCTCCAAC 1080
 DB 475 CCGGTCTCAGCCCGGATGTACAGCTGTGACAGCGCTGCGAGGGGACCCCGCGCTCCAAC 534
 QY 1081 CACTCGGCCAGGACAGCGCGCTGGAGTACCTGCTGCTCTCTCCAAGGCCAAGTTGGTG 1140
 DB 535 CACTCGGCCAGGACAGCGCGCTGGAGTACCTGCTGCTCTCTCCAAGGCCAAGTTGGTG 594
 QY 1141 CCCTCGGAGCGGAGCGCTCCCGGAGCAACAGCTGCCAAGACTCCACGACACCGAGAGC 1200
 DB 595 CCCTCGGAGCGGAGCGCTCCCGGAGCAACAGCTGCCAAGACTCCACGACACCGAGAGC 654
 QY 1201 AACACGAGGAGCAGCGGAGCGCTTATCTACCTGACCAACACATGCGCCGACGCGG 1260
 DB 655 AACACGAGGAGCAGCGGAGCGCTTATCTACCTGACCAACACATGCGCCGACGCGG 714
 QY 1261 CAACGGTCTCGCTCAAGGAGGAGCAGCGGCTTACGACTGCTCGCGCGCGCTCCGAG 1320
 DB 715 CAACGGTCTCGCTCAAGGAGGAGCAGCGGCTTACGACTGCTCGCGCGCGCTCCGAG 774
 QY 1321 AACTCGCAGGCGCGCTCGCGTGTGACGACCGGGGAGCAGATGAAGGTGTACAG 1380
 DB 775 AACTCGCAGGCGCGCTCGCGTGTGACGACCGGGGAGCAGATGAAGGTGTACAG 834
 QY 1381 TCGCAACTGCTCGGCTGCTCTTCTGATCAGCTGTATGATCAGCTCATGATCCACATGGCTGC 1440
 DB 835 TCGCAACTGCTCGGCTGCTCTTCTGATCAGCTGTATGATCAGCTCATGATCCACATGGCTGC 894
 QY 1441 CAGGCTTCCGCTGATCCCTTTTGGAGTGCAAAGTGGCGGTACCCAGCAGGACCGGTAC 1500
 DB 895 CAGGCTTCCGCTGATCCCTTTTGGAGTGCAAAGTGGCGGTACCCAGCAGGACCGGTAC 954
 QY 1501 GAGTTCTCGTCCACATATACCGGAGGAGCAGCGCTTCCACATGAGCTA 1550
 DB 955 GAGTTCTCGTCCACATATACCGGAGGAGCAGCGCTTCCACATGAGCTA 1004

RESULT 14
 ARL149599
 LOCUS ARL149599 1004 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 8 from patent US 6228611.
 ACCESSION ARL149599
 VERSION ARL149599.1 GI:15114190
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE	1 (bases 1 to 1004)	
AUTHORS	Georgopoulos,K.	
TITLE	Ikaros: A T cell pathway regulatory gene	
JOURNAL	Patent: US 6228611-A 8 08-MAY-2001;	
FEATURES	Location/Qualifiers	
source	1..1004	
BASE COUNT	235 a 328 c 286 g 155 t	
ORIGIN	/organism="unknown"	
Query Match	56.0%; Score 868; DB 6; Length 1004;	
Best Local Similarity	88.8%; Pred. No. 6.2e-136;	
Matches 1004; Conservative	0; Mismatches 0; Indels 126; Gaps 1;	
QY	421 GGAGAACGGCCCTTCAGTGCATCAATCAGTCGCGGGCCCTCATTACCCAGAGGGCAACCTG 480	
Db	1 GGAGAACGGCCCTTCAGTGCATCAATCAGTCGCGGGCCCTCATTACCCAGAGGGCAACCTG 60	
QY	481 CTCGGGCACATCAAGCTGCATTCGCGGGAGAGCCCTTCAATGCCACCTCTGCAACTAC 540	
Db	61 CTCGGGCACATCAAGCTGCATTCGCGGGAGAGCCCTTCAATGCCACCTCTGCAACTAC 120	
QY	541 GCCTGCGCGCGGAGGACGCCCTCTACTGCGCCACCTTAGAGAGCACCTCCCTGGTAAACCT 600	
Db	121 GCCTGCGCGCGGAGGACGCCCTCTACTGCGCCACCTTAGAGAGCACCTCC----- 168	
QY	601 CACAAATGTGGATATTGTGGCCGAAGACTATAACACGCGNACCTCTTTAGAGGAACATAA 660	
Db	169 ----- 168	
QY	661 GAGCGCTGCCACAACCTACTTGGAAAGCATGGCCCTTCGCGGCACACTGTACCCAGTCATT 720	
Db	169 -----GTCAAT 174	
QY	721 AAAGAAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 780	
Db	175 AAAGAAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 234	
QY	781 TCTCTCGTGTGCACAGACTAGCACTAATGTGCGCAACAGTAAAGAGTCTATGCTCAG 840	
Db	235 TCTCTCGTGTGCACAGACTAGCACTAATGTGCGCAACAGTAAAGAGTCTATGCTCAG 294	
QY	841 AAATTTCTTTGGGACAAAGGCGCTGTCCGACACGCCCTACGACAGTCCACGATCAGAGAG 900	
Db	295 AAATTTCTTTGGGACAAAGGCGCTGTCCGACACGCCCTACGACAGTCCACGATCAGAGAG 354	
QY	901 GAGAACGAATGATGAAGTCCACAGTGTGACCAAGCCATCAACACGCCATCAACTAC 960	
Db	355 GAGAACGAATGATGAAGTCCACAGTGTGACCAAGCCATCAACACGCCATCAACTAC 414	
QY	961 CTGGGGCCGAGTCCCTGCGCGCGTGGTGCAGACGCCCGCGCGGTTCGAGAGTGGTC 1020	
Db	415 CTGGGGCCGAGTCCCTGCGCGCGTGGTGCAGACGCCCGCGCGGTTCGAGAGTGGTC 474	
QY	1021 CCGGTATATAGCCCGATGTACAGTGCACAGCGCGTTCGAGAGGACACCCCGGCTCCAC 1080	
Db	475 CCGGTATATAGCCCGATGTACAGTGCACAGCGCGTTCGAGAGGACACCCCGGCTCCAC 534	
QY	1081 CACTCGGCCACGACAGCGCGTGGAGTACTCTGCTGTCTCCAAAGCCAAAGTTGGTG 1140	
Db	535 CACTCGGCCACGACAGCGCGTGGAGTACTCTGCTGTCTCCAAAGCCAAAGTTGGTG 594	
QY	1141 CCGTCGGAGCGGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGC 1200	
Db	595 CCGTCGGAGCGGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGC 654	
QY	1201 AACAAAGAGGAGCAGCGCGGTCTTATCTACTGACCAACACATCGCCCGACCGCG 1260	
Db	655 AACAAAGAGGAGCAGCGCGGTCTTATCTACTGACCAACACATCGCCCGACCGCG 714	
QY	1261 CAACGCGTGTGCTCAAGGAGGAGCAGCGCGCTACGACCTGTGCGCGCGCTCCGAG 1320	
Db	194 CATGGGTGAACGGCCTTTCCAGTGCACACAGTGTGGGCCCTTCTTACCCAGAAAGCAA 253	
QY	417 CACTGGAGAACGGCCTTCCAGTGCATCACTGCGGGGCCCTCATTCCACCAAGAGGCAA 476	
Db	194 CATGGGTGAACGGCCTTTCCAGTGCACACAGTGTGGGCCCTTCTTACCCAGAAAGCAA 253	
BASE COUNT	385 a 431 c 423 g 311 t	
ORIGIN		
Query Match	52.5%; Score 814.8; DB 10; Length 1550;	
Best Local Similarity	85.6%; Pred. No. 4.9e-127;	
Matches 984; Conservative	0; Mismatches 142; Indels 24; Gaps 6;	
QY	417 CACTGGAGAACGGCCTTCCAGTGCATCACTGCGGGGCCCTCATTCCACCAAGAGGCAA 476	
Db	194 CATGGGTGAACGGCCTTTCCAGTGCACACAGTGTGGGCCCTTCTTACCCAGAAAGCAA 253	
QY	1321 AACTCCAGGAGCGCGCTCCGCTGGTTCACACACGCGGGAGCAGATGAAGGTGTACAAG 1380	
Db	775 AACTCCAGGAGCGCGCTCCGCTGGTTCACACACGCGGGAGCAGATGAAGGTGTACAAG 834	
QY	1381 TGGGAACACTGCGCGGTGCTCTCTCTGGATCAGTCATGATACACCATCCACATGGGCTGC 1440	
Db	835 TGGGAACACTGCGCGGTGCTCTCTCTGGATCAGTCATGATACACCATCCACATGGGCTGC 894	
QY	1441 CACGGTTCGGTATCCTTTTGTAGTCCAACTGTGCGGGTACACACGACGACCGGTAC 1500	
Db	895 CACGGTTCGGTATCCTTTTGTAGTCCAACTGTGCGGGTACACACGACGACCGGTAC 954	
QY	1501 GAGTTCCTGFCGACATAACGCGGAGGAGCACCGCTTCCACATGAGCTA 1550	
Db	955 GAGTTCCTGFCGACATAACGCGGAGGAGCACCGCTTCCACATGAGCTA 1004	
RESULT 15		
MUSIKAROS		
LOCUS	Mus Ikaros DNA binding protein (Ikaros) mRNA, complete cds.	
DEFINITION	103547.1 GI:198286	
VERSION	DNA-binding transcription factor; Ikaros; Ikaros DNA binding	
KEYWORDS	protein; transcription; zinc finger protein; zinc-finger	
SOURCE	Mus musculus (library: Lambda ZAP EL4) adult cDNA to mRNA.	
ORGANISM	Mus musculus	
REFERENCE	1 (bases 1 to 1550)	
AUTHORS	Georgopoulos,K., Moore,D.D. and Derfler,B.	
TITLE	Ikaros, an early lymphoid-specific transcription factor and a	
JOURNAL	putative mediator for T cell commitment	
MEDLINE	Science 258 (5083), 808-812 (1992)	
FEATURES	93068267 Location/Qualifiers	
source	1..1550	
organism	"Mus musculus"	
db_xref	"taxon:10090"	
cell_type	"T cell"	
dev_stage	"adult"	
tissue_lib	"Lambda ZAP EL4"	
gene	1..1550	
genes	"Ikaros"	
CDS	39..1334	
codon_start	=1	
product	"Ikaros DNA binding protein"	
protein_id	"AA066193.1"	
db_xref	"GI:198287"	
translation	"MDVDEGDMQSVQSGKSPVSDTPDEGDPMPVPEDLSTSCAQ	
QNSKSRGMRGPFQNCQSGATQGNLRLHKHSRKPFCNLCNACRRRLAT		
GHRLTVSGPKHCGKYSYKORSLSEHKRCHNYLESMLPGVCPVKEETNHE		
MAEDLCKIGAESRLVLDRLASNAVKRSKSPQKFLGDKLSDPYDSANYEKEDMTS		
HVMDQALNNAIYVGAESLPVQTPPGSEVVPVSSMVLHKPDPDGPSPRSHSAQ		
DAVDNLLLLKAKSVSSEREASPSNCSQSDTDESNAEORSGLIYLTNHPNPHARG		
LALKEORAYEVLRAASENSODAFRVVYSSTGEOLKYVKECHRCVFLDHWMTIHMG		
HGCHGFRDPFCNMGYHSDRVEFSHITRGEHYHLS"		

QY	477	CTGCTCCGGCACATCAAGCTGCATTTCCGGGAGAGCCCTTCAATGCCACTCTGC	536
DB	254	CTCTCTCCGGCACATCAAGCTGCATCGGCTGAGAGCCCTTCAATGCCACTCTTTG	313
QY	537	CTACGGCTCCGCCGGAGGGAGCCCTTCACTGGCCACTTGAGGACGCACCTCGCTGGTAA	596
DB	314	CTATGCCTCCGCCGGAGGGAGCCCTTCACTGGCCACTTGAGGACGCACCTCGCTGGTAA	373
QY	597	ACCTCACAAATGTGGATATTGTGGCCGAAGCTATAACAGCGGAACGCTTTAGAGGA	656
DB	374	GCCTCACAAATGTGGATATTGTGGCCGAAGCTATAACAGCGGAACGCTTTAGAGGA	433
QY	657	TAAAGAGCGCTGCCACAACACTACTTTGGAAGCATGGGCCCTTCCGGGCACACTGTACCCAGT	716
DB	434	TAAAGAGCGATGCCACAACACTACTTTGGAAGCATGGGCCCTTCCGGGC--GTGTGCCAGT	490
QY	717	CATTAAAGAAAGAACTAAGCACAGTGAATGGCAGAGAACCTGTGCAAGATAGGATCAGA	776
DB	491	CATTAAAGAAAGAACTAACCACAACAGATATGGCAGAAGACCTGTGCAAGATAGGAGCA	550
QY	777	GAGATCTCTCGTGTGCACAGACTAGCAAGTAATGTGCGCAACCTTAAGAGCTCTATGCC	836
DB	551	GAGGTCCCTTTCTCTGTGCACAGGCTGCAAGCAATGTGCGCAACCTTAGAGCTCTATGCC	610
QY	837	TCAGAAATTTCTTGGGCACAAAGGCCCTGTCCGACAGCCCTACGACAGTGCACGTACGA	896
DB	611	TCAGAAATTTCTTGGAGCAAGTGCCTGTGCACATATGCCCTATGACAGTGCACACTATGA	670
QY	897	GAAGGAGAACGAATGATGAAGTCCACAGTATGTGCGCAACCTTAACAGCGGCATCA	956
DB	671	GAAGGAG--GATATGATGACATCCCACTGATGACCAAGCCATCAACAATGGCANTCA	727
QY	957	CTACTTGGGGCCGAGTCCCTGGCGCCGTGTGCAGACGCCCCCGGGCGGTTCCGAGGT	1016
DB	728	CTACTTGGGGCCGAGTCCCTGGCGCCATTTGGTCAGACACCCCGGTAGCTCCGAGGT	787
QY	1017	GGTCCCGGTCTATCAGCCCGATGTACCAGCTGCACAGGG--CTCGGAGGACACCCCGG	1073
DB	788	GGTCCAGTCTATCAGCTCCATGTACAGCTGCACAGCCCCCTTCAGATGGCCCCCGACG	847
QY	1074	CTCCAACCATCTGGCCAGGACAGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1133
DB	848	GTCCAACCATTTACAGCAGGA--CGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	904
QY	1134	GTTGGTCCCTCGGAGCGCGAGCGGTCCCGAGCAACAGTGCACAGCTTCAGGAGCAC	1193
DB	905	GTCTGTGTATCGAGCGAGAGGCGCTCCCGAGCAACAGCTTCGCAAGACTTCCACAGATAC	964
QY	1194	CGAGAGCAACAGGAGGACGCGCGGTCTTATCTACTGACCAACACATATCCCGG	1253
DB	965	AGAGAGCAACGCGGAGGACAGCGAGCGCGGTCTTATCTACTTAACCAACACATCAACC	1024
QY	1254	ACGCGGC--AACGGTGTCTCAAGGAGGACCGCGCTTACGACTGTGTGGCGC	1310
DB	1025	GCATGCACGCAATGGCTGGCTCTCAAGGAGGACGCGCGCTTACGAGTGTGTGGGCG	1084
QY	1311	CGCTCCGAGAACTCGCAGGACGCGCTCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1370
DB	1085	GGCTTCAGAGAACTCGCAGGATGCTTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1144
QY	1371	GGTGTACAAGTCCGAACACTCGCGGTGCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGT	1430
DB	1145	GGTGTACAAGTCCGAACACTCGCGGTGCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGT	1204
QY	1431	CATG-----GGCTGCCACGCTTCCGTGTATCTTTTGTGTGTGTGTGTGTGTGTGTGTGT	1481
DB	1205	CATGGCTGCCATGGCTGCCATGGCTTCCGGATCCCTTGTGTGTGTGTGTGTGTGTGTGT	1264
QY	1482	CCACAGCCAGGACCGTACGATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1541
DB	1265	TCACAGCCAGGACAGGTACGAGTTCTCATCCCATATCAACGCGGGGGAGCATCTGTACCA	1324
QY	1542	CATGAGCTAA	1551

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